

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
Mathur, Brian
Friddle, Carl Johan

<120> Novel Human Kinases and Polynucleotides Encoding the Same

<130> LEX-0332-USA

<150> US 60/282,036

<151> 2001-04-06

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<170> FastSEQ for Windows Version 4.0

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<211> 2337

<212> DNA

<213> homo sapiens

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35 40 45
Lys Leu Gly Val His Cys Ile Thr Gly Gln Lys Val Ala Ile Lys Ile
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Val Asn Arg Glu Lys Leu Ser Glu Ser Val Leu Met Lys Val Glu Arg
65 70 75 80
Glu Ile Ala Ile Leu Lys Leu Ile Glu His Pro His Val Leu Lys Leu
85 90 95
His Asp Val Tyr Glu Asn Lys Lys Tyr Leu Tyr Leu Val Leu Glu His
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Val Ser Gly Gly Glu Leu Phe Asp Tyr Leu Val Lys Lys Gly Arg Leu
115 120 125
Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln Ile Val Ser Ala Leu
130 135 140
Asp Phe Cys His Ser Tyr Ser Ile Cys His Arg Asp Leu Lys Pro Glu
145 150 155 160
Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg Ile Ala Asp Phe Gly
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180 185 190
Ser Pro His Tyr Ala Cys Pro Glu Val Ile Lys Gly Glu Lys Tyr Asp
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Gly Arg Arg Ala Asp Met Trp Ser Cys Gly Val Ile Leu Phe Ala Leu
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Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn Leu Arg Gln Leu Leu
225 230 235 240
Glu Lys Val Lys Arg Gly Val Phe His Met Pro His Phe Ile Pro Pro
245 250 255
Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu Val Glu Pro Glu Lys
260 265 270
Arg Leu Ser Leu Glu Gln Ile Gln Lys His Pro Trp Tyr Leu Gly Gly
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Lys His Glu Pro Asp Pro Cys Leu Glu Pro Ala Pro Gly Arg Arg Val
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Ala Met Arg Ser Leu Pro Ser Asn Gly Glu Leu Asp Pro Asp Val Leu
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Glu Ser Met Ala Ser Leu Gly Cys Phe Arg Asp Arg Glu Arg Leu His
325 330 335

Arg Glu Leu Arg Ser Glu Glu Glu Asn Gln Glu Lys Met Ile Tyr Tyr
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 355 360 365
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 Pro Met Leu Ser Arg His Gly Lys Arg Arg Pro Glu Arg Lys Ser Met
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 Glu Val Leu Ser Ile Thr Asp Ala Gly Gly Gly Gly Ser Pro Val Pro
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 Arg Gly Pro Arg Gly Gly Gly Ala Gly Glu Gln Pro Pro Pro Pro Ser
 485 490 495
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 530 535 540
 Gly Gly Ala Ala Trp Arg Ser Arg Leu Asn Ser Ile Arg Asn Ser Phe
 545 550 555 560
 Leu Gly Ser Pro Arg Phe His Arg Arg Lys Met Gln Val Pro Thr Ala
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 580 585 590
 Arg Ser Trp Phe Gly Asn Phe Ile Ser Leu Asp Lys Glu Glu Gln Ile
 595 600 605
 Phe Leu Val Leu Lys Asp Lys Pro Leu Ser Ser Ile Lys Ala Asp Ile
 610 615 620
 Val His Ala Phe Leu Ser Ile Pro Ser Leu Ser His Ser Val Leu Ser
 625 630 635 640
 Gln Thr Ser Phe Arg Ala Glu Tyr Lys Ala Ser Gly Gly Pro Ser Val
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 Pro Glu Pro Ser Pro Arg Arg Asp Gly Ser Gly Gly Gly Gly Ile Tyr
 675 680 685
 Ser Val Thr Phe Thr Leu Ile Ser Gly Pro Ser Arg Arg Phe Lys Arg
 690 695 700
 Val Val Glu Thr Ile Gln Ala Gln Leu Leu Ser Thr His Asp Gln Pro
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 Ser Val Gln Ala Leu Ala Asp Glu Lys Asn Gly Ala Gln Thr Arg Pro
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Pro Val	Glu Val Gly Asp Glu	Ala Leu Trp Ser Ser	Thr Cys Pro Phe		
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Gln Pro	Ser Ala Pro Ser Ile Ser	Phe Arg Tyr Leu Val	Leu Glu His		
	85	90	95		
Val Ser	Gly Gly Glu Leu Phe Asp	Tyr Leu Val Lys Lys	Gly Arg Leu		
	100	105	110		
Thr Pro	Lys Glu Ala Arg Lys Phe	Phe Arg Gln Ile Val	Ser Ala Leu		
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Asp Phe	Cys His Ser Tyr Ser Ile	Cys His Arg Asp	Leu Lys Pro Glu		
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Asn Leu	Leu Leu Asp Glu Lys	Asn Asn Ile Arg Ile	Ala Asp Phe Gly		
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Ser Pro	His Tyr Ala Cys Pro Glu	Val Ile Lys Gly Glu	Lys Tyr Asp		
	180	185	190		
Gly Arg	Arg Ala Asp Met Trp Ser	Cys Gly Val Ile Leu	Phe Ala Leu		
	195	200	205		
Leu Val	Gly Ala Leu Pro Phe Asp	Asp Asp Asn Leu Arg	Gln Leu Leu		
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Glu Lys	Val Lys Arg Gly Val Phe	His Met Pro His Phe	Ile Pro Pro		
225		230	235		240
Asp Cys	Gln Ser Leu Leu Arg Gly	Met Ile Glu Val Glu	Pro Glu Lys		
	245	250	255		
Arg Leu	Ser Leu Glu Gln Ile Gln	Lys His Pro Trp Tyr	Leu Gly Gly		
	260	265	270		
Lys His	Glu Pro Asp Pro Cys Leu	Glu Pro Ala Pro Gly	Arg Arg Val		
	275	280	285		
Ala Met	Arg Ser Leu Pro Ser Asn	Gly Glu Leu Asp Pro	Asp Val Leu		
290		295	300		
Glu Ser	Met Ala Ser Leu Gly	Cys Phe Arg Asp Arg	Glu Arg Leu His		
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Arg Glu	Leu Arg Ser Glu Glu Glu	Asn Gln Glu Lys Met	Ile Tyr Tyr		
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	355	360	365		
Pro Met	Leu Ser Arg His Gly Lys	Arg Arg Pro Glu Arg	Lys Ser Met		
	370	375	380		
Glu Val	Leu Ser Ile Thr Asp	Ala Gly Gly Gly Ser	Pro Val Pro		
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Thr Arg	Arg Ala Leu Glu Met	Ala Gln His Ser Gln	Arg Ser Arg Ser		
	405	410	415		
Val Ser	Gly Ala Ser Thr Gly Leu	Ser Ser Ser Pro Leu	Ser Ser Pro		
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Arg Ser	Pro Val Phe Ser Phe Ser	Pro Glu Pro Gly Ala	Gly Asp Glu		
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Thr Gly Thr Pro	Gly Thr Thr Pro	Pro Pro Ser Pro	Gly Gly Gly Val			
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Gly Gly Ala Ala	Trp Arg Ser Arg	Leu Asn Ser Ile	Arg Asn Ser Phe			
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Val His Ala Phe	Leu Ser Ile Pro	Ser Leu Ser His	Ser Val Leu Ser			
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Gln Thr Ser Phe	Arg Ala Glu Tyr	Lys Ala Ser Gly	Gly Gly Pro Ser			
625	630	635	640			
Phe Gln Lys Pro	Val Arg Phe Gln	Val Asp Ile Ser	Ser Ser Ser Glu			
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Pro Glu Pro Ser	Pro Arg Arg Asp	Gly Ser Gly Gly	Gly Gly Ile Tyr			
	660	665	670			
Ser Val Thr Phe	Thr Leu Ile Ser	Gly Pro Ser Arg	Arg Phe Lys Arg			
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Val Val Glu Thr	Ile Gln Ala Gln	Leu Leu Ser Thr	His Asp Gln Pro			
	690	695	700			
Ser Val Gln Ala	Leu Ala Asp Glu	Lys Asn Gly Ala	Gln Thr Arg Pro			
705	710	715	720			
Ala Gly Ala Pro	Pro Arg Ser Leu	Gln Pro Pro Gly	Arg Pro Asp			
	725	730	735			
Pro Glu Leu Ser	Ser Ser Pro Arg	Arg Gly Pro Pro	Lys Asp Lys Lys			
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 <212> DNA
 <213> homo sapiens

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<210> 6
<211> 703
<212> PRT
<213> homo sapiens

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35 40 45
Lys Lys Gly Arg Leu Thr Pro Lys Glu Ala Arg Lys Phe Phe Arg Gln
50 55 60
Ile Val Ser Ala Leu Asp Phe Cys His Ser Tyr Ser Ile Cys His Arg
65 70 75 80
Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu Lys Asn Asn Ile Arg
85 90 95
Ile Ala Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu
100 105 110
Glu Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Val Ile Lys
115 120 125
Gly Glu Lys Tyr Asp Gly Arg Arg Ala Asp Met Trp Ser Cys Gly Val
130 135 140
Ile Leu Phe Ala Leu Leu Val Gly Ala Leu Pro Phe Asp Asp Asp Asn
145 150 155 160
Leu Arg Gln Leu Leu Glu Lys Val Lys Arg Gly Val Phe His Met Pro
165 170 175
His Phe Ile Pro Pro Asp Cys Gln Ser Leu Leu Arg Gly Met Ile Glu
180 185 190

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Val	Glu	Pro	Glu	Lys	Arg	Leu	Ser	Leu	Glu	Gln	Ile	Gln	Lys	His	Pro	195	200	205
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Pro	Gly	Arg	Arg	Val	Ala	Met	Arg	Ser	Leu	Pro	Ser	Asn	Gly	Glu	Leu	225	230	235
Asp	Pro	Asp	Val	Leu	Glu	Ser	Met	Ala	Ser	Leu	Gly	Cys	Phe	Arg	Asp	245	250	255
Arg	Glu	Arg	Leu	His	Arg	Glu	Leu	Arg	Ser	Glu	Glu	Glu	Asn	Gln	Glu	260	265	270
Lys	Met	Ile	Tyr	Tyr	Leu	Leu	Leu	Asp	Arg	Lys	Glu	Arg	Tyr	Pro	Ser	275	280	285
Cys	Glu	Asp	Gln	Asp	Leu	Pro	Pro	Arg	Asn	Asp	Val	Asp	Pro	Pro	Arg	290	295	300
Lys	Arg	Val	Asp	Ser	Pro	Met	Leu	Ser	Arg	His	Gly	Lys	Arg	Arg	Pro	305	310	315
Glu	Arg	Lys	Ser	Met	Glu	Val	Leu	Ser	Ile	Thr	Asp	Ala	Gly	Gly	Gly	325	330	335
Gly	Ser	Pro	Val	Pro	Thr	Arg	Arg	Ala	Leu	Glu	Met	Ala	Gln	His	Ser	340	345	350
Gln	Arg	Ser	Arg	Ser	Val	Ser	Gly	Ala	Ser	Thr	Gly	Leu	Ser	Ser	Ser	355	360	365
Pro	Leu	Ser	Ser	Pro	Arg	Ser	Pro	Val	Phe	Ser	Phe	Ser	Pro	Glu	Pro	370	375	380
Gly	Ala	Gly	Asp	Glu	Ala	Arg	Gly	Gly	Gly	Ser	Pro	Thr	Ser	Lys	Thr	385	390	395
Gln	Thr	Leu	Pro	Ser	Arg	Gly	Pro	Arg	Gly	Gly	Gly	Ala	Gly	Glu	Gln	405	410	415
Pro	Pro	Pro	Pro	Ser	Ala	Arg	Ser	Thr	Pro	Leu	Pro	Gly	Pro	Pro	Gly	420	425	430
Ser	Pro	Arg	Ser	Ser	Gly	Gly	Thr	Pro	Leu	His	Ser	Pro	Leu	His	Thr	435	440	445
Pro	Arg	Ala	Ser	Pro	Thr	Gly	Thr	Pro	Gly	Thr	Thr	Pro	Pro	Pro	Ser	450	455	460
Pro	Gly	Gly	Gly	Val	Gly	Gly	Ala	Ala	Trp	Arg	Ser	Arg	Leu	Asn	Ser	465	470	475
Ile	Arg	Asn	Ser	Phe	Leu	Gly	Ser	Pro	Arg	Phe	His	Arg	Arg	Lys	Met	485	490	495
Gln	Val	Pro	Thr	Ala	Glu	Glu	Met	Ser	Ser	Leu	Thr	Pro	Glu	Ser	Ser	500	505	510
Pro	Glu	Leu	Ala	Lys	Arg	Ser	Trp	Phe	Gly	Asn	Phe	Ile	Ser	Leu	Asp	515	520	525
Lys	Glu	Glu	Gln	Ile	Phe	Leu	Val	Leu	Lys	Asp	Lys	Pro	Leu	Ser	Ser	530	535	540
Ile	Lys	Ala	Asp	Ile	Val	His	Ala	Phe	Leu	Ser	Ile	Pro	Ser	Leu	Ser	545	550	555
His	Ser	Val	Leu	Ser	Gln	Thr	Ser	Phe	Arg	Ala	Glu	Tyr	Lys	Ala	Ser	565	570	575
Gly	Gly	Pro	Ser	Val	Phe	Gln	Lys	Pro	Val	Arg	Phe	Gln	Val	Asp	Ile	580	585	590
Ser	Ser	Ser	Glu	Gly	Pro	Glu	Pro	Ser	Pro	Arg	Arg	Asp	Gly	Ser	Gly	595	600	605
Gly	Gly	Gly	Ile	Tyr	Ser	Val	Thr	Phe	Thr	Leu	Ile	Ser	Gly	Pro	Ser	610	615	620
Arg	Arg	Phe	Lys	Arg	Val	Val	Glu	Thr	Ile	Gln	Ala	Gln	Leu	Leu	Ser	625	630	635

Thr	His	Asp	Gln	Pro	Ser	Val	Gln	Ala	Leu	Ala	Asp	Glu	Lys	Asn	Gly
				645					650					655	
Ala	Gln	Thr	Arg	Pro	Ala	Gly	Ala	Pro	Pro	Arg	Ser	Leu	Gln	Pro	Pro
			660					665					670		
Pro	Gly	Arg	Pro	Asp	Pro	Glu	Leu	Ser	Ser	Ser	Pro	Arg	Arg	Gly	Pro
		675					680					685			
Pro	Lys	Asp	Lys	Lys	Leu	Leu	Ala	Thr	Asn	Gly	Thr	Pro	Leu	Pro	
	690					695					700				